

Resource Summary Report

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SAGE GENIE

RRID:SCR_000796

Type: Tool

Proper Citation

SAGE GENIE (RRID:SCR_000796)

Resource Information

URL: <http://cgap.nci.nih.gov/SAGE/AnatomicViewer>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 9, 2022. The SAGE Genie website provides highly intuitive, visual displays of human and mouse gene expression, based on a unique analytical process (Boon et al.) that reliably matches SAGE tags, 10 or 17 nucleotides in length, to known genes. Recently, with the construction and incorporation of a reference database of SNP-associated alternative tags into SAGE Genie (Silva et al.), the interpretation of tag to human gene mapping has been enhanced. Human SAGE Genie Tools The SAGE Anatomic Viewer visually displays the relative expression of a given gene in normal and malignant tissues of the human body. In addition, there is access to: o The Digital Northern, which shows the relative expression of the gene in each library. o The Ludwig Transcript (LT) Viewer, which visually represents a particular transcript with up to four possible virtual SAGE tag locations (starting from the 3' end) and locations of internally primed or alternatively polyadenylated transcripts. o Expanded access to brain, hES cells, and breast cell subtypes. * The SAGE Digital Gene Expression Displayer distinguishes significant differences in gene expression profiles between two pools of SAGE libraries. * The SAGE Experimental Viewer provides DGED results for pre-set pairs of libraries, one under control and the other under experimental conditions. * The SAGE Absolute Level Lister lists all SAGE libraries and links to the distribution of transcript expression levels in any given library. * The SAGE Library Finder tool searches for one or more tissue-specific libraries from the SAGE collection. * SAGE Genie Downloads provide files of genes, tags, datasets, mappings, and more. * SAGE Genomics Finder tool searches for genomics info for tags. * DKView tool for viewing Digital Karyotyping data. * DK Microbe tool searches for exact matches of 17 base-pair digital karyotyping tags in bacterial and viral genomes. * SAGE Tag Extraction tool to extract tags from sequence files. Mouse SAGE Genie Tools * The mSAGE Expression Matrix visually displays the relative expression of a given gene through stages of mouse development. In addition, there is access to: o The Digital Northern, which shows the relative expression of the gene in each library. o The Ludwig Transcript (LT) Viewer, which visually represents a particular transcript with up to four

possible virtual SAGE tag locations (starting from the 3' end) and locations of internally primed or alternatively polyadenylated transcripts. * The mSAGE Absolute Level Lister lists all mouse SAGE libraries, organized by either tissue (normal or malignant) or developmental stage, and links to the distribution of transcript expression levels in any given library. * The mSAGE Digital Gene Expression Displayer distinguishes significant differences in gene expression profiles between two pools of mouse SAGE libraries. * The mSAGE Experimental Viewer automatically sets up the DGED with mouse libraries, prepared as stand alone experiments, for gene expression comparison. * The mSAGE Library Finder tool searches for one or more tissue-specific mouse libraries from the SAGE collection. * mSAGE Genie Downloads provide files of mouse genes, tags, datasets, mappings, and more. * SAGE Genomics Finder tool searches for genomics info for tags. * SAGE Tag Extraction tool to extract tags from sequence files. Notes: The majority of human libraries are short whereas the majority of mouse libraries are long. Several mouse developmental libraries are prepared by the SAGELite method. SAGELite is an extension of the long Sage protocol that includes a PCR-based amplification stage to allow the use of 10ng to 100ng of total RNA to produce a Sage library. However, it has been observed that a significant bias incurred by this amplification process. SAGE Genie was produced as part of the NCI CGAP SAGE project with collaborators from Johns Hopkins University, the Ludwig Institute for Cancer Research, Sao Paulo Branch, the University of Texas MD Anderson Cancer Center, and the Genome Sciences Center of the BCCRC.

Synonyms: SAGE GENIE

Resource Type: data or information resource, database

Defining Citation: [PMID:12119410](#)

Keywords: molecular neuroanatomy resource

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SAGE GENIE

Resource ID: SCR_000796

Alternate IDs: nif-0000-31482

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260905T133112+0000

Ratings and Alerts

No rating or validation information has been found for SAGE GENIE.

No alerts have been found for SAGE GENIE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Li M, et al. (2020) Key genes with prognostic values in suppression of osteosarcoma metastasis using comprehensive analysis. BMC cancer, 20(1), 65.

Li M, et al. (2020) Comprehensive Analysis of Key Genes and Regulatory Elements in Osteosarcoma Affected by Bone Matrix Mineral With Prognostic Values. Frontiers in genetics, 11, 533.

Pan W, et al. (2014) CSBF/C10orf99, a novel potential cytokine, inhibits colon cancer cell growth through inducing G1 arrest. Scientific reports, 4, 6812.

Kraiklang R, et al. (2014) A novel predictive equation for potential diagnosis of cholangiocarcinoma. PloS one, 9(2), e89337.

Sengoelge G, et al. (2014) A SAGE based approach to human glomerular endothelium: defining the transcriptome, finding a novel molecule and highlighting endothelial diversity. BMC genomics, 15(1), 725.

Freitas M, et al. (2013) Expression of cancer/testis antigens is correlated with improved survival in glioblastoma. Oncotarget, 4(4), 636.

Zhu H, et al. (2013) Over-expression of the ATP5J gene correlates with cell migration and 5-fluorouracil sensitivity in colorectal cancer. PloS one, 8(10), e76846.

Zhang Y, et al. (2009) DNA methylation analysis of chromosome 21 gene promoters at single base pair and single allele resolution. PLoS genetics, 5(3), e1000438.

Wu JQ, et al. (2008) Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. Genome biology, 9(1), R3.

Gierke P, et al. (2004) Expression analysis of members of the neuronal calcium sensor protein family: combining bioinformatics and Western blot analysis. Biochemical and biophysical research communications, 323(1), 38.

Pyle AD, et al. (2004) Chipping away at 'stemness'. Genome biology, 5(8), 235.